What Is Claimed Is:

1. A recombinant lambdoid bacteriophage vector comprising a nucleotide sequence that (i) defines the lambdoid elements for replication and packaging of the vector into an assembled bacteriophage, and (ii) encodes a conditionally suppressible cistron for expression of a tail protein and a fusion protein that comprises:

a) a promoter for transcribing the cistron,

b) a first upstream translatable sequence that encodes a lambdoid bacteriophage tail polypeptide,

c) a first ribosome binding site to initiate translation of said upstream translatable sequence,

d) a second translatable sequence operatively linked downstream to said first translatable sequence that (i) encodes a linker polypeptide in frame with said tail polypeptide and (ii) includes a sequence adapted for ligation of an insert polynucleotide that defines a third translatable sequence downstream from said second translatable sequence that encodes a preselected polypeptide, and

e) a suppressor termination codon within said second translatable sequence that upon suppression results in read-through to form a fusion polypeptide consisting of said tail polypeptide, linker polypeptide and preselected polypeptide.

2. The vector of claim 1 wherein said second translatable sequence further includes a nucleotide sequence that defines a second ribosome binding site to initiate translation of said third translatable sequence.

3. The vector of claim 1 wherein said lambdoid bacteriophage tail polypeptide is selected from the group consisting of pJ, pV, pG, pM and pT.

4. The vector of claim 1 wherein said lambdoid

bacteriophage tail polypeptide is pV.

5. The vector of claim 4 wherein said pV includes residues 1-176 of the amino acid residue sequence shown in SEQ ID NO 6, and conservative substitutions thereof.

6. The vector of claim 1 wherein said suppressor termination codon is selected from the group consisting of the amber and opal codons.

7. The vector of claim 1 wherein said linker polypeptide is from about 10 ~~to~~ about 100 amino acids in length.

8. The vector of claim ~~1~~ wherein said linker polypeptide has a amino acid residue sequence from 178 to 213 as shown in SEQ ID NO 6.

9. The vector of claim 1 wherein said conditionally suppressible cistron has a nucleotide sequence shown in SEQ ID NO 5.

10. The vector of claim 1 wherein said vector has a nucleotide sequence functionally similar to the sequence of λfoo having ATCC accession number ____.

11. A recombinant lambdoid bacteriophage comprising a matrix of proteins encapsulating a lambdoid genome encoding a fusion protein, said matrix including said fusion protein surface accessible in said matrix, and said fusion protein consisting essentially of, in the direction of amino terminus to carboxy terminus, a lambdoid bacteriophage tail polypeptide, a linker polypeptide and a preselected polypeptide.

12. The lambdoid bacteriophage of claim 11 wherein said lambdoid bacteriophage tail polypeptide is selected from the group consisting of pJ, pV, pG, pM and pT.

13. The lambdoid bacteriophage vector of claim 11 wherein said lambdoid bacteriophage tail

polypeptide is pV.

14. The lambdoid bacteriophage of claim 13 wherein said pV includes residues 1-176 of the amino acid residue sequence shown in SEQ ID NO 1, and conservative substitutions thereof.

15. The lambdoid bacteriophage of claim 11 wherein said preselected polypeptide defines a biologically active protein selected from the group consisting of an enzyme, a ligand and a receptor.

16. The lambdoid bacteriophage of claim 11 wherein said lambdoid genome further encodes a heterologous protein capable of forming a multimeric protein complex with said fusion protein in said matrix.

17. The lambdoid bacteriophage of claim 11 wherein said fusion protein is present as a multimeric protein.

18. The lambdoid bacteriophage of claim 17 wherein said multimeric protein is selected from the group consisting of beta-galactosidase and Bauhinia purpurea agglutinin.

19. The lambdoid bacteriophage of claim 11 wherein said linker polypeptide has an amino acid residue sequence from 178 to 213 as shown in SEQ ID NO 6.

20. The lambdoid bacteriophage of claim 11 wherein said bacteriophage is detectably labeled.

21. A fusion protein having an amino acid residue sequence that comprises, in the direction of amino terminus to carboxy terminus, a lambdoid bacteriophage tail polypeptide, a linker polypeptide and a preselected polypeptide defining a biological activity.

22. A library of recombinant lambdoid bacteriophage particles wherein each particle contains

a recombinant lambdoid bacteriophage vector according to claim 1.

23. The library of claim 22 wherein said library contains at least 10^7 different species of said vector.

24. A library of recombinant lambdoid bacteriophage particles wherein each particle comprises a matrix of proteins encapsulating a lambdoid genome, said matrix including a fusion protein according to claim 21 surface accessible in said matrix.

25. A method for detecting the presence of a preselected target in a sample comprising the steps of:

a) admixing a sample containing said preselected target with a recombinant lambdoid bacteriophage according to claim 15, wherein said preselected polypeptide defines a biologically active ligand or receptor able to bind said preselected target, under binding conditions sufficient for said target-binding bacteriophage to bind said target and form a target-ligand or receptor complex;

b) detecting the presence of said complex, and thereby the presence of said preselected target.

26. The method of claim 25 wherein said detecting comprises detecting the presence of said bacteriophage particles, and thereby the presence of said preselected target.

27. A method for producing a recombinant lambdoid bacteriophage, comprising the steps of:

a) infecting an E. coli host strain having a termination codon suppression phenotype with a recombinant lambdoid bacteriophage vector according to claim 1; and

b) culturing said infected host strain

under bacteriophage growth conditions to produce said recombinant lambdoid bacteriophage.

28. The method of claim 27 wherein said E. coli host strain is selected from the group consisting of EQ166, CA168 and MC8.

29. The method of claim 28 wherein said MC8 has the characteristics of ATCC accession number ____.

add c2 cll D17